

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Stojiljkovic, Igor
So, Magdalene
Hwa, Vivian
Heffron, Fred
Nassif, Xavier

(ii) TITLE OF INVENTION: Novel Bacterial Hemoglobin Receptor
Genes and Uses

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
(B) STREET: 300 South Wacker Drive, 32nd Floor
(C) CITY: Chicago
(D) STATE: Illinois
(E) COUNTRY: USA
(F) ZIP: 60606

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/537,361
(B) FILING DATE: 02-OCT-1995
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Noonan, Kevin E
(B) REGISTRATION NUMBER: 35,303
(C) REFERENCE/DOCKET NUMBER: 94,784-A

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 312-913-0001
(B) TELEFAX: 312-913-0002

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3319 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 471..2848

006160" 85E59560
Jul
B1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGAACTAGTG GATCCAATTT GGGCGCGGCG TTTTGTTC A	AACACGCCCA AAAACTCGAT	60
TACAACGGCG AACACGGCGC GCGCCACCTC GCTCCGCATC	CCGACGGGCC GCGGCAAACA	120
CTGGCGCGCC TTCGTCGAGC ATCTTGAACG CTTTGAACCT	GACTCCCGAA GCCGAAGCGG	180
AAGCCATTCA AGGCGCGCGC GAAGCCTTTG CATTCTACAA	AGTCGTGTTG CGCGAAACCT	240
TCGGCTTGGC AGCCGATGCC GAAGCCCCCG AAGGTATGAT	GCCGCACAGG CACTAAAAAA	300
TAATCGAACC AAATAAACAA GGTCTCGGCA TAGCTGTTTG	CAGGGACCTT TAATTACAG	360
GCGCGGCTTT GTTTACATGG ATTACTGTCT TATTAAATAT	TAATGATTAT CATAAAATCT	420
ATTATTCGCT AACCGATGGA TGAACAATCC ATACATCTTG	AGTTGATAAT ATG AAA	476
	Met Lys	
	1	
CCA TTA CAA ATG CTC CCT ATC GCC GCG CTG GTC	GGC AGT ATT TTC GGC	524
Pro Leu Gln Met Leu Pro Ile Ala Ala Leu Val	Gly Ser Ile Phe Gly	
5	10 15	
AAT CCG GTC TTT GCG GCA GAT GAA GCT GCA ACT	GAA ACC ACA CCC GTT	572
Asn Pro Val Phe Ala Ala Asp Glu Ala Ala Thr	Glu Thr Thr Pro Val	
20	25 30	
AAG GCA GAG GTA AAA GCA GTG CGC GGT AAA GGC	CAG CGC AAT GCG CCT	620
Lys Ala Glu Val Lys Ala Val Arg Gly Lys Gly	Gln Arg Asn Ala Pro	
35	40 45 50	
GCG GCT GTG GAA CGC GTC AAC CTT AAC CGT ATC	AAA CAA GAA ATG ATA	668
Ala Ala Val Glu Arg Val Asn Leu Asn Arg Ile	Lys Gln Glu Met Ile	
55	60 65	
CGC GAC AAC AAA GAC TTG GTG CGC TAT TCC ACC	GAT GTC GGC TTG AGC	716
Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr	Asp Val Gly Leu Ser	
70	75 80	
GAC AGC GGC CGC CAT CAA AAA GGC TTT GCT GTT	CGC GGC GTG GAA GGC	764
Asp Ser Gly Arg His Gln Lys Gly Phe Ala Val	Arg Gly Val Glu Gly	
85	90 95	
AAC CGT GTC GGC GTG AGC ATA GAC GGC GTA AAC	CTG CCT GAT TCC GAA	812
Asn Arg Val Gly Val Ser Ile Asp Gly Val Asn	Leu Pro Asp Ser Glu	
100	105 110	
GAA AAC TCG CTG TAC GCC CGT TAT GGC AAC TTC	AAC AGC TCG CGT CTG	860
Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe	Asn Ser Ser Arg Leu	
115	120 125 130	
TCT ATC GAC CCC GAA CTC GTG CGC AAC ATC GAC	ATC GTA AAA GGG GCG	908
Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Asp	Ile Val Lys Gly Ala	
135	140 145	
GAC TCT TTC AAT ACC GGC AGC GGC GCC TTG GGC	GGC GGT GTG AAT TAC	956
Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly	Gly Gly Val Asn Tyr	

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			150				155				160							
CAA	ACC	CTG	CAA	GGA	CGT	GAC	TTA	CTG	TTG	CCT	GAA	CGG	CAG	TTC	GGC	1004		
Gln	Thr	Leu	Gln	Gly	Arg	Asp	Leu	Leu	Leu	Pro	Glu	Arg	Gln	Phe	Gly			
			165				170				175							
GTG	ATG	ATG	AAA	AAC	GGT	TAC	AGC	ACG	CGT	AAC	CGT	GAA	TGG	ACA	AAT	1052		
Val	Met	Met	Lys	Asn	Gly	Tyr	Ser	Thr	Arg	Asn	Arg	Glu	Trp	Thr	Asn			
			180				185				190							
ACC	CTC	GGT	TTC	GGC	GTG	AGC	AAC	GAC	CGC	GTG	GAT	GCC	GCT	TTG	CTG	1100		
Thr	Leu	Gly	Phe	Gly	Val	Ser	Asn	Asp	Arg	Val	Asp	Ala	Ala	Leu	Leu			
			195				200				205				210			
TAT	TCG	CAA	CGG	CGC	GGC	CAT	GAA	ACT	GAA	AGC	GCG	GGC	AAG	CGT	GGT	1148		
Tyr	Ser	Gln	Arg	Arg	Gly	His	Glu	Thr	Glu	Ser	Ala	Gly	Lys	Arg	Gly			
			215				220				225							
TAT	CCG	GTA	GAG	GGT	GCT	GGT	AGC	GGA	GCG	AAT	ATC	CGT	GGT	TCT	GCG	1196		
Tyr	Pro	Val	Glu	Gly	Ala	Gly	Ser	Gly	Ala	Asn	Ile	Arg	Gly	Ser	Ala			
			230				235				240							
CGC	GGT	ATT	CCT	GAT	CCG	TCC	CAA	CAC	AAA	TAC	CAC	AGC	TTC	TTG	GGT	1244		
Arg	Gly	Ile	Pro	Asp	Pro	Ser	Gln	His	Lys	Tyr	His	Ser	Phe	Leu	Gly			
			245				250				255							
AAG	ATT	GCT	TAT	CAA	ATC	AAC	GAC	AAC	CAC	CGC	ATC	GGC	GCA	TCG	CTC	1292		
Lys	Ile	Ala	Tyr	Gln	Ile	Asn	Asp	Asn	His	Arg	Ile	Gly	Ala	Ser	Leu			
			260				265				270							
AAC	GGT	CAG	CAG	GGG	CAT	AAT	TAC	ACG	GTT	GAA	GAG	TCT	TAC	AAC	CTG	1340		
Asn	Gly	Gln	Gln	Gly	His	Asn	Tyr	Thr	Val	Glu	Glu	Ser	Tyr	Asn	Leu			
			275				280				285				290			
CTT	GCT	TCT	TAT	TGG	CGT	GAA	GCT	GAC	GAT	GTC	AAC	AGA	CGG	CGT	AAC	1388		
Leu	Ala	Ser	Tyr	Trp	Arg	Glu	Ala	Asp	Asp	Val	Asn	Arg	Arg	Arg	Asn			
			295				300				305							
ACC	AAC	CTC	TTT	TAC	GAA	TGG	ACG	CCG	GAA	TCC	GAC	CGG	TTG	TCT	ATG	1436		
Thr	Asn	Leu	Phe	Tyr	Glu	Trp	Thr	Pro	Glu	Ser	Asp	Arg	Leu	Ser	Met			
			310				315				320							
GTA	AAA	GCG	GAT	GTC	GAT	TAT	CAA	AAA	ACC	AAA	GTA	TCT	GCG	GTC	AAC	1484		
Val	Lys	Ala	Asp	Val	Asp	Tyr	Gln	Lys	Thr	Lys	Val	Ser	Ala	Val	Asn			
			325				330				335							
TAC	AAA	GGT	TCG	TTC	CCG	ATA	GAG	GAT	TCT	TCC	ACC	TTG	ACA	CGT	AAC	1532		
Tyr	Lys	Gly	Ser	Phe	Pro	Ile	Glu	Asp	Ser	Ser	Thr	Leu	Thr	Arg	Asn			
			340				345				350							
TAC	AAT	CAA	AAG	GAC	TTG	GAT	GAA	ATC	TAC	AAC	CGC	AGT	ATG	GAT	ACC	1580		
Tyr	Asn	Gln	Lys	Asp	Leu	Asp	Glu	Ile	Tyr	Asn	Arg	Ser	Met	Asp	Thr			
			355				360				365				370			
CGC	TTC	AAA	CGC	ATT	ACC	CTG	CGT	TTG	GAC	AGC	CAT	CCG	TTG	CAA	CTC	1628		
Arg	Phe	Lys	Arg	Ile	Thr	Leu	Arg	Leu	Asp	Ser	His	Pro	Leu	Gln	Leu			
			375				380				385							
GGG	GGG	GGG	CGA	CAC	CGC	CTG	TCG	TTT	AAA	ACT	TTC	GCC	AGC	CGC	CGT	1676		

Gly	Gly	Gly	Arg	His	Arg	Leu	Ser	Phe	Lys	Thr	Phe	Ala	Ser	Arg	Arg		
			390					395					400				
GAT	TTT	GAA	AAC	CTA	AAC	CGC	GAC	GAT	TAT	TAC	TTC	AGC	GGC	CGT	GTT	1724	
Asp	Phe	Glu	Asn	Leu	Asn	Arg	Asp	Asp	Tyr	Tyr	Phe	Ser	Gly	Arg	Val		
		405					410					415					
GTT	CGA	ACC	ACC	AGC	AGT	ATC	CAG	CAT	CCG	GTG	AAA	ACC	ACC	AAC	TAC	1772	
Val	Arg	Thr	Thr	Ser	Ser	Ile	Gln	His	Pro	Val	Lys	Thr	Thr	Asn	Tyr		
		420				425					430						
GGT	TTC	TCA	CTG	TCT	GAC	CAA	ATT	CAA	TGG	AAC	GAC	GTG	TTC	AGT	AGC	1820	
Gly	Phe	Ser	Leu	Ser	Asp	Gln	Ile	Gln	Trp	Asn	Asp	Val	Phe	Ser	Ser		
					440				445						450		
CGC	GCA	GGT	ATC	CGT	TAC	GAT	CAT	ACC	AAA	ATG	ACG	CCT	CAG	GAA	TTG	1868	
Arg	Ala	Gly	Ile	Arg	Tyr	Asp	His	Thr	Lys	Met	Thr	Pro	Gln	Glu	Leu		
				455					460					465			
AAT	GCC	GAG	TGT	CAT	GCT	TGT	GAC	AAA	ACA	CCG	CCT	GCA	GCC	AAC	ACT	1916	
Asn	Ala	Glu	Cys	His	Ala	Cys	Asp	Lys	Thr	Pro	Pro	Ala	Ala	Asn	Thr		
			470					475					480				
TAT	AAA	GGC	TGG	AGC	GGT	TTT	GTC	GGC	TTG	GCG	GCG	CAA	CTG	AAT	CAG	1964	
Tyr	Lys	Gly	Trp	Ser	Gly	Phe	Val	Gly	Leu	Ala	Ala	Gln	Leu	Asn	Gln		
		485					490					495					
GCT	TGG	CGT	GTC	GGT	TAC	GAC	ATT	ACT	TCC	GGC	TAC	CGT	GTC	CCC	AAT	2012	
Ala	Trp	Arg	Val	Gly	Tyr	Asp	Ile	Thr	Ser	Gly	Tyr	Arg	Val	Pro	Asn		
		500				505					510						
GCG	TCC	GAA	GTG	TAT	TTC	ACT	TAC	AAC	CAC	GGT	TCG	GGT	AAT	TGG	CTG	2060	
Ala	Ser	Glu	Val	Tyr	Phe	Thr	Tyr	Asn	His	Gly	Ser	Gly	Asn	Trp	Leu		
		515				520				525					530		
CCC	AAT	CCC	AAC	CTG	AAA	GCC	GAG	CGC	ACG	ACC	ACC	CAC	ACC	CTC	TCT	2108	
Pro	Asn	Pro	Asn	Leu	Lys	Ala	Glu	Arg	Thr	Thr	Thr	His	Thr	Leu	Ser		
				535					540					545			
CTG	CAA	GGC	CGC	AGC	GAA	AAA	GGT	ACT	TTG	GAT	GCC	AAC	CTG	TAT	CAA	2156	
Leu	Gln	Gly	Arg	Ser	Glu	Lys	Gly	Thr	Leu	Asp	Ala	Asn	Leu	Tyr	Gln		
			550					555					560				
AGC	AAT	TAC	CGC	AAT	TTC	CTG	TCT	GAA	GAG	CAG	AAG	CTG	ACC	ACC	AGC	2204	
Ser	Asn	Tyr	Arg	Asn	Phe	Leu	Ser	Glu	Glu	Gln	Lys	Leu	Thr	Thr	Ser		
		565					570					575					
GGC	GAT	GTC	AGC	TGT	ACT	CAG	ATG	AAT	TAC	TAC	TAC	GGT	ATG	TGT	AGC	2252	
Gly	Asp	Val	Ser	Cys	Thr	Gln	Met	Asn	Tyr	Tyr	Tyr	Gly	Met	Cys	Ser		
		580				585					590						
AAT	CCT	TAT	TCC	GAA	AAA	CTG	GAA	TGG	CAG	ATG	CAA	AAT	ATC	GAC	AAG	2300	
Asn	Pro	Tyr	Ser	Glu	Lys	Leu	Glu	Trp	Gln	Met	Gln	Asn	Ile	Asp	Lys		
					600				605					610			
GCC	AGA	ATC	CGC	GGT	ATC	GAG	CTG	ACG	GGC	CGT	CTG	AAT	GTG	GAC	AAA	2348	
Ala	Arg	Ile	Arg	Gly	Ile	Glu	Leu	Thr	Gly	Arg	Leu	Asn	Val	Asp	Lys		
				615					620					625			

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GTA GCG TCT TTT GTT CCT GAG GGC TGG AAA CTG TTC GGC TCG CTG GGT Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser Leu Gly 630 635 640	2396
TAT GCG AAA AGC AAA CTG TCG GGC GAC AAC AGC CTG CTG TTC ACC CAG Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Phe Thr Gln 645 650 655	2444
CCG TTG AAA GTG ATT GCC GGT ATC GAC TAT GAA AGT CCG AGC GAA AAA Pro Leu Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser Glu Lys 660 665 670	2492
TGG GGC GTG TTC TCC CGC CTG ACC TAT CTG GGC GCG AAA AAG GTC AAA Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys Val Lys 675 680 685 690	2540
GAC GCG CAA TAC ACC GTT TAT GAA AAC AAG GGC TGG GGT ACG CCT TTG Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Trp Gly Thr Pro Leu 695 700 705	2588
CAG AAA AAG GTA AAA GAT TAC CCG TGG CTG AAC AAG TCG GCT TAT GTG Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala Tyr Val 710 715 720	2636
TTC GAT ATG TAC GGC TTC TAC AAA CCG GTG AAA AAC CTG ACT TTG CGT Phe Asp Met Tyr Gly Phe Tyr Lys Pro Val Lys Asn Leu Thr Leu Arg 725 730 735	2684
GCA GGC GTA TAT AAT GTG TTC AAC CGC AAA TAC ACC ACT TGG GAT TCC Ala Gly Val Tyr Asn Val Phe Asn Arg Lys Tyr Thr Thr Trp Asp Ser 740 745 750	2732
CTG CGC GGC CTG TAT AGC TAC AGC ACC ACC AAC TCG GTC GAC CGC GAT Leu Arg Gly Leu Tyr Ser Tyr Ser Thr Thr Asn Ser Val Asp Arg Asp 755 760 765 770	2780
GGC AAA GGC TTA GAC CGC TAC CGC GCC CCA AGC CGT AAT TAC GCC GTA Gly Lys Gly Leu Asp Arg Tyr Arg Ala Pro Ser Arg Asn Tyr Ala Val 775 780 785	2828
TCG CTG GAA TGG AAG TTT TA ATCTGGTATT ATTGAATTAA TCGCCTTGTT Ser Leu Glu Trp Lys Phe 790	2878
GAAAATTAAA GCCGTCCGAA TTGTGTTCAA GAACTCATTC GGACGGTTTT TACCGAATCT	2938
GTGTGTGGGT TTATAGTGGA TTAACAAAAA TCAGGACAAG GCGACGAAGC CGCAGACAGT	2998
ACAGATAGTA CGGAACCGAT TCACTTGGTG AGACCTTTGC AAAATTCCTT TCCCTCCCGA	3058
CAGCCGAAAC CCAAACACAG GTTTTCGGCT GTTTTCGCCC CAAATACCTC CTAATTCTAC	3118
CCAAATACCC CCTTAATCCT CCCCATAACC CGATAATCAG GCATCCGGCG CCTTTAGGCG	3178
GCAGCGGGCG CACTTAACCT GTTGCGGGCT TTCAAAGGT TCAAACACAT CGCCTTCAGG	3238
TGCCTTTGCG CACTCACTTT AATCAGTCCG AAATAGGCCG CCCGCGCATA GCAGAACTTA	3298
CGGTGCAGCG TACCGAAGCT T	3319

0065358-091900

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 792 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Pro Leu Gln Met Leu Pro Ile Ala Ala Leu Val Gly Ser Ile
1 5 10 15
Phe Gly Asn Pro Val Phe Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr
20 25 30
Pro Val Lys Ala Glu Val Lys Ala Val Arg Gly Lys Gly Gln Arg Asn
35 40 45
Ala Pro Ala Ala Val Glu Arg Val Asn Leu Asn Arg Ile Lys Gln Glu
50 55 60
Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly
65 70 75 80
Leu Ser Asp Ser Gly Arg His Gln Lys Gly Phe Ala Val Arg Gly Val
85 90 95
Glu Gly Asn Arg Val Gly Val Ser Ile Asp Gly Val Asn Leu Pro Asp
100 105 110
Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser
115 120 125
Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Asp Ile Val Lys
130 135 140
Gly Ala Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly Gly Gly Val
145 150 155 160
Asn Tyr Gln Thr Leu Gln Gly Arg Asp Leu Leu Leu Pro Glu Arg Gln
165 170 175
Phe Gly Val Met Met Lys Asn Gly Tyr Ser Thr Arg Asn Arg Glu Trp
180 185 190
Thr Asn Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala
195 200 205
Leu Leu Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Lys
210 215 220
Arg Gly Tyr Pro Val Glu Gly Ala Gly Ser Gly Ala Asn Ile Arg Gly
225 230 235 240
Ser Ala Arg Gly Ile Pro Asp Pro Ser Gln His Lys Tyr His Ser Phe

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	245		250		255
Leu Gly Lys	Ile Ala Tyr Gln Ile	Asn Asp Asn His Arg	Ile Gly Ala		
	260	265	270		
Ser Leu Asn	Gly Gln Gln Gly His	Asn Tyr Thr Val Glu	Glu Ser Tyr		
	275	280	285		
Asn Leu Leu	Ala Ser Tyr Trp Arg	Glu Ala Asp Asp	Val Asn Arg Arg		
	290	295	300		
Arg Asn Thr	Asn Leu Phe Tyr Glu	Trp Thr Pro Glu	Ser Asp Arg Leu		
305	310	315	320		
Ser Met Val	Lys Ala Asp Val Asp	Tyr Gln Lys Thr	Lys Val Ser Ala		
	325	330	335		
Val Asn Tyr	Lys Gly Ser Phe Pro	Ile Glu Asp Ser	Ser Thr Leu Thr		
	340	345	350		
Arg Asn Tyr	Asn Gln Lys Asp Leu	Asp Glu Ile Tyr	Asn Arg Ser Met		
	355	360	365		
Asp Thr Arg	Phe Lys Arg Ile Thr	Leu Arg Leu Asp	Ser His Pro Leu		
	370	375	380		
Gln Leu Gly	Gly Gly Arg His Arg	Leu Ser Phe Lys	Thr Phe Ala Ser		
385	390	395	400		
Arg Arg Asp	Phe Glu Asn Leu Asn	Arg Asp Asp Tyr	Tyr Phe Ser Gly		
	405	410	415		
Arg Val Val	Arg Thr Thr Ser Ser	Ile Gln His Pro	Val Lys Thr Thr		
	420	425	430		
Asn Tyr Gly	Phe Ser Leu Ser Asp	Gln Ile Gln Trp	Asn Asp Val Phe		
	435	440	445		
Ser Ser Arg	Ala Gly Ile Arg Tyr	Asp His Thr Lys	Met Thr Pro Gln		
	450	455	460		
Glu Leu Asn	Ala Glu Cys His Ala	Cys Asp Lys Thr	Pro Pro Ala Ala		
465	470	475	480		
Asn Thr Tyr	Lys Gly Trp Ser Gly	Phe Val Gly Leu	Ala Ala Gln Leu		
	485	490	495		
Asn Gln Ala	Trp Arg Val Gly Tyr	Asp Ile Thr Ser	Gly Tyr Arg Val		
	500	505	510		
Pro Asn Ala	Ser Glu Val Tyr Phe	Thr Tyr Asn His	Gly Ser Gly Asn		
	515	520	525		
Trp Leu Pro	Asn Pro Asn Leu Lys	Ala Glu Arg Thr	Thr Thr His Thr		
	530	535	540		
Leu Ser Leu	Gln Gly Arg Ser Glu	Lys Gly Thr Leu	Asp Ala Asn Leu		
545	550	555	560		

006T60" 85E5960

Tyr Gln Ser Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Lys Leu Thr
 565 570 575
 Thr Ser Gly Asp Val Ser Cys Thr Gln Met Asn Tyr Tyr Tyr Gly Met
 580 585 590
 Cys Ser Asn Pro Tyr Ser Glu Lys Leu Glu Trp Gln Met Gln Asn Ile
 595 600 605
 Asp Lys Ala Arg Ile Arg Gly Ile Glu Leu Thr Gly Arg Leu Asn Val
 610 615 620
 Asp Lys Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser
 625 630 635
 Leu Gly Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Phe
 645 650 655
 Thr Gln Pro Leu Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser
 660 665 670
 Glu Lys Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys
 675 680 685
 Val Lys Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Trp Gly Thr
 690 695 700
 Pro Leu Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala
 705 710 715 720
 Tyr Val Phe Asp Met Tyr Gly Phe Tyr Lys Pro Val Lys Asn Leu Thr
 725 730 735
 Leu Arg Ala Gly Val Tyr Asn Val Phe Asn Arg Lys Tyr Thr Thr Trp
 740 745 750
 Asp Ser Leu Arg Gly Leu Tyr Ser Tyr Ser Thr Thr Asn Ser Val Asp
 755 760 765
 Arg Asp Gly Lys Gly Leu Asp Arg Tyr Arg Ala Pro Ser Arg Asn Tyr
 770 775 780
 Ala Val Ser Leu Glu Trp Lys Phe
 785 790

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2376 base pairs
 - (B) TYPE: nucleic acid

006160" 85559950

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..2373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG AAA CCA TTA CAA ATG CCC CCT ATC GCC GCG CTG CTC GGC AGT ATT	48
Met Lys Pro Leu Gln Met Pro Pro Ile Ala Ala Leu Leu Gly Ser Ile	
1 5 10 15	
TTC GGC AAT CCG GTC TTT GCG GCA GAT GAA GCT GCA ACT GAA ACC ACA	96
Phe Gly Asn Pro Val Phe Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr	
20 25 30	
CCC GTT AAG GCA GAG GTA AAA GCA GTG CGC GTT AAA GGT CAG CGC AAT	144
Pro Val Lys Ala Glu Val Lys Ala Val Arg Val Lys Gly Gln Arg Asn	
35 40 45	
GCG CCT GCG GCT GTG GAA CGC GTC AAC CTT AAC CGT ATC AAA CAA GAA	192
Ala Pro Ala Ala Val Glu Arg Val Asn Leu Asn Arg Ile Lys Gln Glu	
50 55 60	
ATG ATA CGC GAC AAT AAA GAC TTG GTG CGC TAT TCC ACC GAT GTC GGC	240
Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly	
65 70 75 80	
TTG AGC GAC AGG AGC CGT CAT CAA AAA GGC TTT GCC ATT CGC GGC GTG	288
Leu Ser Asp Arg Ser Arg His Gln Lys Gly Phe Ala Ile Arg Gly Val	
85 90 95	
GAA GGC GAC CGT GTC GGC GTT AGT ATT GAC GGC GTA AAC CTG CCT GAT	336
Glu Gly Asp Arg Val Gly Val Ser Ile Asp Gly Val Asn Leu Pro Asp	
100 105 110	
TCC GAA GAA AAC TCG CTG TAC GCC CGT TAT GGC AAC TTC AAC AGC TCG	384
Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser	
115 120 125	
CGT CTG TCT ATC GAC CCC GAA CTC GTG CGC AAC ATC GAC ATC GTA AAA	432
Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Asp Ile Val Lys	
130 135 140	
GGG GCG GAC TCT TTC AAT ACC GGC AGC GGC GCC TTG GGC GGC GGT GTG	480
Gly Ala Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly Gly Gly Val	
145 150 155 160	
AAT TAC CAA ACC CTG CAA GGA CGT GAC TTA CTG TTG CCT GAA CGG CAG	528
Asn Tyr Gln Thr Leu Gln Gly Arg Asp Leu Leu Leu Pro Glu Arg Gln	
165 170 175	
TTC GGC GTG ATG ATG AAA AAC GGT TAC AGC ACG CGT AAC CGT GAA TGG	576
Phe Gly Val Met Met Lys Asn Gly Tyr Ser Thr Arg Asn Arg Glu Trp	
180 185 190	

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ACA	AAT	ACC	CTC	GGT	TTC	GGC	GTG	AGC	AAC	GAC	CGC	GTG	GAT	GCC	GCT	624
Thr	Asn	Thr	Leu	Gly	Phe	Gly	Val	Ser	Asn	Asp	Arg	Val	Asp	Ala	Ala	
	195						200					205				
TTG	CTG	TAT	TCG	CAA	CGG	CGC	GGC	CAT	GAA	ACT	GAA	AGC	GCG	GGC	AAG	672
Leu	Leu	Tyr	Ser	Gln	Arg	Arg	Gly	His	Glu	Thr	Glu	Ser	Ala	Gly	Lys	
	210						215					220				
CGT	GGT	TAT	CCG	GTA	GAG	GGT	GCT	GGT	AGC	GGA	GCG	AAT	ATC	CGT	GGT	720
Arg	Gly	Tyr	Pro	Val	Glu	Gly	Ala	Gly	Ser	Gly	Ala	Asn	Ile	Arg	Gly	
	225						230					235			240	
TCT	GCG	CGC	GGT	ATT	CCT	GAT	CCG	TCC	CAA	CAC	AAA	TAC	CAC	AGC	TTC	768
Ser	Ala	Arg	Gly	Ile	Pro	Asp	Pro	Ser	Gln	His	Lys	Tyr	His	Ser	Phe	
				245											255	
TTG	GGT	AAG	ATT	GCT	TAT	CAA	ATC	AAC	GAC	AAC	CAC	CGC	ATC	GGC	GCA	816
Leu	Gly	Lys	Ile	Ala	Tyr	Gln	Ile	Asn	Asp	Asn	His	Arg	Ile	Gly	Ala	
			260										270			
TCG	CTC	AAC	GGT	CAG	CAG	GGG	CAT	AAT	TAC	ACG	GTT	GAA	GAG	TCT	TAC	864
Ser	Leu	Asn	Gly	Gln	Gln	Gly	His	Asn	Tyr	Thr	Val	Glu	Glu	Ser	Tyr	
			275										285			
AAC	CTG	CTT	GCT	TCT	TAT	TGG	CGT	GAA	GCT	GAC	GAT	GTC	AAC	AGA	CGG	912
Asn	Leu	Leu	Ala	Ser	Tyr	Trp	Arg	Glu	Ala	Asp	Asp	Val	Asn	Arg	Arg	
	290						295					300				
CGT	AAC	ACC	AAC	CTC	TTT	TAC	GAA	TGG	ACG	CCG	GAA	TCC	GAC	CGG	TTG	960
Arg	Asn	Thr	Asn	Leu	Phe	Tyr	Glu	Trp	Thr	Pro	Glu	Ser	Asp	Arg	Leu	
	305					310						315			320	
TCT	ATG	GTA	AAA	GCG	GAT	GTC	GAT	TAT	CAA	AAA	ACC	AAA	GTA	TCT	GCG	1008
Ser	Met	Val	Lys	Ala	Asp	Val	Asp	Tyr	Gln	Lys	Thr	Lys	Val	Ser	Ala	
				325											335	
GTC	AAC	TAC	AAA	GGT	TCG	TTC	CCG	ACG	AAT	TAC	ACC	ACA	TGG	GAA	ACC	1056
Val	Asn	Tyr	Lys	Gly	Ser	Phe	Pro	Thr	Asn	Tyr	Thr	Thr	Trp	Glu	Thr	
			340										350			
GAG	TAC	CAT	AAA	AAG	GAA	GTT	GGC	GAA	ATC	TAT	AAC	CGC	AGC	ATG	GAT	1104
Glu	Tyr	His	Lys	Lys	Glu	Val	Gly	Glu	Ile	Tyr	Asn	Arg	Ser	Met	Asp	
			355										365			
ACA	ACC	TTC	AAA	CGT	ATT	ACG	CTG	CGT	ATG	GAC	AGC	CAT	CCG	TTG	CAA	1152
Thr	Thr	Phe	Lys	Arg	Ile	Thr	Leu	Arg	Met	Asp	Ser	His	Pro	Leu	Gln	
	370						375					380				
CTC	GGG	GGG	GGG	CGA	CAC	CGC	CTG	TCG	TTT	AAA	ACC	TTT	GCC	GGG	CAG	1200
Leu	Gly	Gly	Gly	Arg	His	Arg	Leu	Ser	Phe	Lys	Thr	Phe	Ala	Gly	Gln	
	385						390								400	
CGT	GAT	TTT	GAA	AAC	TTA	AAC	CGC	GAC	GAT	TAC	TAC	TTC	AGC	GGC	CGT	1248
Arg	Asp	Phe	Glu	Asn	Leu	Asn	Arg	Asp	Asp	Tyr	Tyr	Phe	Ser	Gly	Arg	
				405						410				415		
GTT	GTT	CGA	ACC	ACC	AAC	AGT	ATC	CAG	CAT	CCG	GTG	AAA	ACC	ACC	AAC	1296
Val	Val	Arg	Thr	Thr	Asn	Ser	Ile	Gln	His	Pro	Val	Lys	Thr	Thr	Asn	
			420							425				430		

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TAC	GGT	TTC	TCG	CTG	TCC	GAC	CAA	ATC	CAA	TGG	AAC	GAC	GTG	TTC	AGT	1344
Tyr	Gly	Phe	Ser	Leu	Ser	Asp	Gln	Ile	Gln	Trp	Asn	Asp	Val	Phe	Ser	
	435						440					445				
AGC	CGC	GCA	GGT	ATC	CGT	TAC	GAC	CAC	ACC	AAA	ATG	ACG	CCT	CAG	GAA	1392
Ser	Arg	Ala	Gly	Ile	Arg	Tyr	Asp	His	Thr	Lys	Met	Thr	Pro	Gln	Glu	
	450					455					460					
TTG	AAT	GCC	GAC	TGT	CAT	GCT	TGT	GAC	AAA	ACA	CCG	CCT	GCA	GCC	AAC	1440
Leu	Asn	Ala	Asp	Cys	His	Ala	Cys	Asp	Lys	Thr	Pro	Pro	Ala	Ala	Asn	
465					470				475						480	
ACT	TAT	AAA	GGC	TGG	AGC	GGA	TTT	GTC	GGC	TTG	GCG	GCG	CAG	CTG	AGC	1488
Thr	Tyr	Lys	Gly	Trp	Ser	Gly	Phe	Val	Gly	Leu	Ala	Ala	Gln	Leu	Ser	
			485						490					495		
CAA	ACA	TGG	CGT	TTG	GGT	TAC	GAT	GTG	ACC	TCA	GGT	TTC	CGC	GTG	CCG	1536
Gln	Thr	Trp	Arg	Leu	Gly	Tyr	Asp	Val	Thr	Ser	Gly	Phe	Arg	Val	Pro	
			500					505					510			
AAT	GCG	TCT	GAA	GTG	TAT	TTC	ACT	TAC	AAC	CAC	GGT	TCG	GGC	ACT	TGG	1584
Asn	Ala	Ser	Glu	Val	Tyr	Phe	Thr	Tyr	Asn	His	Gly	Ser	Gly	Thr	Trp	
	515						520					525				
AAG	CCT	AAT	CCT	AAT	TTG	AAG	GCA	GAA	CGC	AGC	ACC	ACC	CAC	ACC	CTG	1632
Lys	Pro	Asn	Pro	Asn	Leu	Lys	Ala	Glu	Arg	Ser	Thr	Thr	His	Thr	Leu	
	530					535					540					
TCC	TTG	CAG	GGG	CGC	GGC	GAC	AAA	GGG	ACA	CTG	GAT	GCC	AAC	CTG	TAT	1680
Ser	Leu	Gln	Gly	Arg	Gly	Asp	Lys	Gly	Thr	Leu	Asp	Ala	Asn	Leu	Tyr	
545					550				555						560	
CAA	AGC	AAT	TAC	CGA	AAC	TTC	CTG	TCG	GAA	GAG	CAG	AAT	CTG	ACT	GTC	1728
Gln	Ser	Asn	Tyr	Arg	Asn	Phe	Leu	Ser	Glu	Glu	Gln	Asn	Leu	Thr	Val	
				565					570					575		
AGC	GGC	ACA	CCC	GGC	TGT	ACT	GAG	GAG	GAT	GCT	TAC	TAC	TAT	AGA	TGC	1776
Ser	Gly	Thr	Pro	Gly	Cys	Thr	Glu	Glu	Asp	Ala	Tyr	Tyr	Tyr	Arg	Cys	
			580					585					590			
AGC	GAC	CCC	TAC	AAA	GAA	AAA	CTG	GAT	TGG	CAG	ATG	AAA	AAT	ATC	GAC	1824
Ser	Asp	Pro	Tyr	Lys	Glu	Lys	Leu	Asp	Trp	Gln	Met	Lys	Asn	Ile	Asp	
		595					600					605				
AAG	GCC	AGA	ATC	CGC	GGT	ATC	GAG	TTG	ACA	GGC	CGT	CTG	AAT	GTG	GAC	1872
Lys	Ala	Arg	Ile	Arg	Gly	Ile	Glu	Leu	Thr	Gly	Arg	Leu	Asn	Val	Asp	
	610					615					620					
AAA	GTA	GCG	TCT	TTT	GTT	CCT	GAG	GGT	TGG	AAA	CTG	TTC	GGC	TCG	CTG	1920
Lys	Val	Ala	Ser	Phe	Val	Pro	Glu	Gly	Trp	Lys	Leu	Phe	Gly	Ser	Leu	
625					630				635						640	
GGT	TAT	GCG	AAA	AGC	AAA	CTG	TCG	GGC	GAC	AAC	AGC	CTG	CTG	TCC	ACA	1968
Gly	Tyr	Ala	Lys	Ser	Lys	Leu	Ser	Gly	Asp	Asn	Ser	Leu	Leu	Ser	Thr	
				645					650					655		
CAG	CCG	CTG	AAA	GTG	ATT	GCC	GGT	ATC	GAC	TAT	GAA	AGT	CCG	AGC	GAA	2016
Gln	Pro	Leu	Lys	Val	Ile	Ala	Gly	Ile	Asp	Tyr	Glu	Ser	Pro	Ser	Glu	
			660					665					670			

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AAA TGG GGC GTA TTC TCC CGC CTG ACC TAT CTA GGC GCG AAA AAG GTC	2064
Lys Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys Val	
675 680 685	
AAA GAC GCG CAA TAC ACC GTT TAT GAA AAC AAG GGC TGG GGT ACG CCT	2112
Lys Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Trp Gly Thr Pro	
690 695 700	
TTG CAG AAA AAG GTA AAA GAT TAC CCG TGG CTG AAC AAG TCG GCT TAT	2160
Leu Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala Tyr	
705 710 715 720	
GTG TTT GAT ATG TAC GGC TTC TAC AAA CCG GCT AAA AAC CTG ACT TTG	2208
Val Phe Asp Met Tyr Gly Phe Tyr Lys Pro Ala Lys Asn Leu Thr Leu	
725 730 735	
CGT GCA GGC GTG TAC AAC CTG TTC AAC CGC AAA TAC ACC ACT TGG GAT	2256
Arg Ala Gly Val Tyr Asn Leu Phe Asn Arg Lys Tyr Thr Thr Trp Asp	
740 745 750	
TCC CTG CGC GGT TTA TAT AGC TAC AGC ACC ACC AAT GCG GTC GAC CGC	2304
Ser Leu Arg Gly Leu Tyr Ser Tyr Ser Thr Thr Asn Ala Val Asp Arg	
755 760 765	
GAT GGC AAA GGC TTA GAC CGC TAC CGC GCC CCA GGC CGC AAT TAC GCC	2352
Asp Gly Lys Gly Leu Asp Arg Tyr Arg Ala Pro Gly Arg Asn Tyr Ala	
770 775 780	
GTA TCG CTG GAA TGG AAG TTT TAA	2376
Val Ser Leu Glu Trp Lys Phe	
785 790	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Lys Pro Leu Gln Met Pro Pro Ile Ala Ala Leu Leu Gly Ser Ile	
1 5 10 15	
Phe Gly Asn Pro Val Phe Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr	
20 25 30	
Pro Val Lys Ala Glu Val Lys Ala Val Arg Val Lys Gly Gln Arg Asn	
35 40 45	
Ala Pro Ala Ala Val Glu Arg Val Asn Leu Asn Arg Ile Lys Gln Glu	
50 55 60	
Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly	
65 70 75 80	

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Leu Ser Asp Arg Ser Arg His Gln Lys Gly Phe Ala Ile Arg Gly Val
85 90 95

Glu Gly Asp Arg Val Gly Val Ser Ile Asp Gly Val Asn Leu Pro Asp
100 105 110

Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser
115 120 125

Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Asp Ile Val Lys
130 135 140

Gly Ala Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly Gly Gly Val
145 150 155 160

Asn Tyr Gln Thr Leu Gln Gly Arg Asp Leu Leu Leu Pro Glu Arg Gln
165 170 175

Phe Gly Val Met Met Lys Asn Gly Tyr Ser Thr Arg Asn Arg Glu Trp
180 185 190

Thr Asn Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala
195 200 205

Leu Leu Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Lys
210 215 220

Arg Gly Tyr Pro Val Glu Gly Ala Gly Ser Gly Ala Asn Ile Arg Gly
225 230 235 240

Ser Ala Arg Gly Ile Pro Asp Pro Ser Gln His Lys Tyr His Ser Phe
245 250 255

Leu Gly Lys Ile Ala Tyr Gln Ile Asn Asp Asn His Arg Ile Gly Ala
260 265 270

Ser Leu Asn Gly Gln Gln Gly His Asn Tyr Thr Val Glu Glu Ser Tyr
275 280 285

Asn Leu Leu Ala Ser Tyr Trp Arg Glu Ala Asp Asp Val Asn Arg Arg
290 295 300

Arg Asn Thr Asn Leu Phe Tyr Glu Trp Thr Pro Glu Ser Asp Arg Leu
305 310 315 320

Ser Met Val Lys Ala Asp Val Asp Tyr Gln Lys Thr Lys Val Ser Ala
325 330 335

Val Asn Tyr Lys Gly Ser Phe Pro Thr Asn Tyr Thr Thr Trp Glu Thr
340 345 350

Glu Tyr His Lys Lys Glu Val Gly Glu Ile Tyr Asn Arg Ser Met Asp
355 360 365

Thr Thr Phe Lys Arg Ile Thr Leu Arg Met Asp Ser His Pro Leu Gln
370 375 380

Leu Gly Gly Gly Arg His Arg Leu Ser Phe Lys Thr Phe Ala Gly Gln
385 390 395 400

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Arg Asp Phe Clu Asn Leu Asn Arg Asp Asp Tyr Tyr Phe Ser Gly Arg
405 410 415

Val Val Arg Thr Thr Asn Ser Ile Gln His Pro Val Lys Thr Thr Asn
420 425 430

Tyr Gly Phe Ser Leu Ser Asp Gln Ile Gln Trp Asn Asp Val Phe Ser
435 440 445

Ser Arg Ala Gly Ile Arg Tyr Asp His Thr Lys Met Thr Pro Gln Glu
450 455 460

Leu Asn Ala Asp Cys His Ala Cys Asp Lys Thr Pro Pro Ala Ala Asn
465 470 475 480

Thr Tyr Lys Gly Trp Ser Gly Phe Val Gly Leu Ala Ala Gln Leu Ser
485 490 495

Gln Thr Trp Arg Leu Gly Tyr Asp Val Thr Ser Gly Phe Arg Val Pro
500 505 510

Asn Ala Ser Glu Val Tyr Phe Thr Tyr Asn His Gly Ser Gly Thr Trp
515 520 525

Lys Pro Asn Pro Asn Leu Lys Ala Glu Arg Ser Thr Thr His Thr Leu
530 535 540

Ser Leu Gln Gly Arg Gly Asp Lys Gly Thr Leu Asp Ala Asn Leu Tyr
545 550 555 560

Gln Ser Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Asn Leu Thr Val
565 570 575

Ser Gly Thr Pro Gly Cys Thr Glu Glu Asp Ala Tyr Tyr Tyr Arg Cys
580 585 590

Ser Asp Pro Tyr Lys Glu Lys Leu Asp Trp Gln Met Lys Asn Ile Asp
595 600 605

Lys Ala Arg Ile Arg Gly Ile Glu Leu Thr Gly Arg Leu Asn Val Asp
610 615 620

Lys Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser Leu
625 630 635 640

Gly Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Ser Thr
645 650 655

Gln Pro Leu Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser Glu
660 665 670

Lys Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys Val
675 680 685

Lys Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Trp Gly Thr Pro
690 695 700

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Leu Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala Tyr
705 710 715 720

Val Phe Asp Met Tyr Gly Phe Tyr Lys Pro Ala Lys Asn Leu Thr Leu
725 730 735

Arg Ala Gly Val Tyr Asn Leu Phe Asn Arg Lys Tyr Thr Thr Trp Asp
740 745 750

Ser Leu Arg Gly Leu Tyr Ser Tyr Ser Thr Thr Asn Ala Val Asp Arg
755 760 765

Asp Gly Lys Gly Leu Asp Arg Tyr Arg Ala Pro Gly Arg Asn Tyr Ala
770 775 780

Val Ser Leu Glu Trp Lys Phe
785 790

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2379 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..2376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG AAA CCA TTA CAA ATG CTC CCT ATC GCC GCG CTG GTC GGC AGT ATT	48
Met Lys Pro Leu Gln Met Leu Pro Ile Ala Ala Leu Val Gly Ser Ile	
1 5 10 15	
TTC GGC AAT CCG GTC TTT GCG GCA GAT GAA GCT GCA ACT GAA ACC ACA	96
Phe Gly Asn Pro Val Phe Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr	
20 25 30	
CCC GTT AAG GCA GAG GTA AAA GCA GTG CGC GTT AAA GGC CAG CGC AAT	144
Pro Val Lys Ala Glu Val Lys Ala Val Arg Val Lys Gly Gln Arg Asn	
35 40 45	
GCG CCT GCG GCT GTG GAA CGC GTC AAC CTT AAC CGT ATC AAA CAA GAA	192
Ala Pro Ala Ala Val Glu Arg Val Asn Leu Asn Arg Ile Lys Gln Glu	
50 55 60	
ATG ATA CGC GAC AAC AAA GAC TTG GTG CGC TAT TCC ACC GAT GTC GGC	240
Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly	
65 70 75 80	
TTG AGC GAC AGC GGC CGC CAT CAA AAA GGC TTT GCC GTT CGC GGC GTG	288
Leu Ser Asp Ser Gly Arg His Gln Lys Gly Phe Ala Val Arg Gly Val	
85 90 95	

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GAA GGC AAC CGT GTC GGC GTG AGC ATA GAC GGC GTA AAC CTG CCT GAT	336
Glu Gly Asn Arg Val Gly Val Ser Ile Asp Gly Val Asn Leu Pro Asp	
100 105 110	
TCC GAA GAA AAC TCG CTG TAC GCC CGT TAT GGC AAC TTC AAC AGC TCG	384
Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser	
115 120 125	
CGT CTG TCT ATC GAC CCC GAA CTC GTG CGC AAC ATC GAC ATC GTA AAA	432
Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Asp Ile Val Lys	
130 135 140	
GGG GCG GAC TCT TTC AAT ACC GGC AGC GGC GCC TTG GGC GGC GGT GTG	480
Gly Ala Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly Gly Gly Val	
145 150 155 160	
AAT TAC CAA ACC CTG CAA GGA CGT GAC TTA CTG TTG CCT GAA CGG CAG	528
Asn Tyr Gln Thr Leu Gln Gly Arg Asp Leu Leu Leu Pro Glu Arg Gln	
165 170 175	
TTC GGC GTG ATG ATG AAA AAC GGT TAC AGC ACG CGT AAC CGT GAA TGG	576
Phe Gly Val Met Met Lys Asn Gly Tyr Ser Thr Arg Asn Arg Glu Trp	
180 185 190	
ACA AAT ACC CTC GGT TTC GGC GTG AGC AAC GAC CGC GTG GAT GCC GCT	624
Thr Asn Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala	
195 200 205	
TTG CTG TAT TCG CAA CGG CGC GGC CAT GAA ACT GAA AGC GCG GGC AAG	672
Leu Leu Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Lys	
210 215 220	
CGT GGT TAT CCG GTA GAG GGT GCT GGT AGC GGA GCG AAT ATC CGT GGT	720
Arg Gly Tyr Pro Val Glu Gly Ala Gly Ser Gly Ala Asn Ile Arg Gly	
225 230 235 240	
TCT GCG CGC GGT ATT CCT GAT CCG TCC CAA CAC AAA TAC CAC AGC TTC	768
Ser Ala Arg Gly Ile Pro Asp Pro Ser Gln His Lys Tyr His Ser Phe	
245 250 255	
TTG GGT AAG ATT GCT TAT CAA ATC AAC GAC AAC CAC CGC ATC GGC GCA	816
Leu Gly Lys Ile Ala Tyr Gln Ile Asn Asp Asn His Arg Ile Gly Ala	
260 265 270	
TCG CTC AAC GGT CAG CAG GGG CAT AAT TAC ACG GTT GAA GAG TCT TAC	864
Ser Leu Asn Gly Gln Gln Gly His Asn Tyr Thr Val Glu Glu Ser Tyr	
275 280 285	
AAC CTG CTT GCT TCT TAT TGG CGT GAA GCT GAC GAT GTC AAC AGA CGG	912
Asn Leu Leu Ala Ser Tyr Trp Arg Glu Ala Asp Asp Val Asn Arg Arg	
290 295 300	
CGT AAC ACC AAC CTC TTT TAC GAA TGG ACG CCG GAA TCC GAC CGG TTG	960
Arg Asn Thr Asn Leu Phe Tyr Glu Trp Thr Pro Glu Ser Asp Arg Leu	
305 310 315 320	
TCT ATG GTA AAA GCG GAT GTC GAT TAT CAA AAA ACC AAA GTA TCT GCG	1008
Ser Met Val Lys Ala Asp Val Asp Tyr Gln Lys Thr Lys Val Ser Ala	
325 330 335	

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GTC AAC TAC AAA GGT TCG TTC CCG ATA GAG GAT TCT TCC ACC TTG ACA	1056
Val Asn Tyr Lys Gly Ser Phe Pro Ile Glu Asp Ser Ser Thr Leu Thr	
340 345 350	
CGT AAC TAC AAT CAA AAG GAC TTG GAT GAA ATC TAC AAC CGC AGT ATG	1104
Arg Asn Tyr Asn Gln Lys Asp Leu Asp Glu Ile Tyr Asn Arg Ser Met	
355 360 365	
GAT ACC CGC TTC AAA CGT ATT ACG CTG CGT TTG GAC AGC CAT CCG TTG	1152
Asp Thr Arg Phe Lys Arg Ile Thr Leu Arg Leu Asp Ser His Pro Leu	
370 375 380	
CAA CTC GGG GGG GGG CGA CAC CGC CTG TCG TTT AAA ACT TTC GCC AGC	1200
Gln Leu Gly Gly Gly Arg His Arg Leu Ser Phe Lys Thr Phe Ala Ser	
385 390 395 400	
CGC CGT GAT TTT GAA AAC CTA AAC CGC GAC TAT TAC TAC TTC AGC GGC	1248
Arg Arg Asp Phe Glu Asn Leu Asn Arg Asp Tyr Tyr Tyr Phe Ser Gly	
405 410 415	
CGT GTT GTT CGA ACC ACC AGC AGT ATC CAG CAT CCG GTG AAA ACC ACC	1296
Arg Val Val Arg Thr Thr Ser Ser Ile Gln His Pro Val Lys Thr Thr	
420 425 430	
AAC TAC GGT TTC TCA CTG TCT GAC CAA ATT CAA TGG AAC GAC GTG TTC	1344
Asn Tyr Gly Phe Ser Leu Ser Asp Gln Ile Gln Trp Asn Asp Val Phe	
435 440 445	
AGT AGC CGC GCA GGT ATC CGT TAC GAT CAT ACC AAA ATG ACG CCT CAG	1392
Ser Ser Arg Ala Gly Ile Arg Tyr Asp His Thr Lys Met Thr Pro Gln	
450 455 460	
GAA TTG AAT GCC GAG TGT CAT GCT TGT GAC AAA ACA CCG CCT GCA GCC	1440
Glu Leu Asn Ala Glu Cys His Ala Cys Asp Lys Thr Pro Pro Ala Ala	
465 470 475 480	
AAC ACT TAT AAA GGC TGG AGC GGT TTT GTC GGC TTG GCG GCG CAA CTG	1488
Asn Thr Tyr Lys Gly Trp Ser Gly Phe Val Gly Leu Ala Ala Gln Leu	
485 490 495	
AAT CAG GCT TGG CGT GTC GGT TAC GAC ATT ACT TCC GGC TAC CGT GTC	1536
Asn Gln Ala Trp Arg Val Gly Tyr Asp Ile Thr Ser Gly Tyr Arg Val	
500 505 510	
CCC AAT GCG TCC GAA GTG TAT TTC ACT TAC AAC CAC GGT TCG GGT AAT	1584
Pro Asn Ala Ser Glu Val Tyr Phe Thr Tyr Asn His Gly Ser Gly Asn	
515 520 525	
TGG CTG CCC AAT CCC AAC CTG AAA GCC GAG CGC ACG ACC ACC CAC ACC	1632
Trp Leu Pro Asn Pro Asn Leu Lys Ala Glu Arg Thr Thr Thr His Thr	
530 535 540	
CTC TCT CTG CAA GGC CGC AGC GAA AAA GGT ACT TTG GAT GCC AAC CTG	1680
Leu Ser Leu Gln Gly Arg Ser Glu Lys Gly Thr Leu Asp Ala Asn Leu	
545 550 555 560	
TAT CAA AGC AAT TAC CGA AAT TTC CTG TCT GAA GAG CAG AAG CTG ACC	1728
Tyr Gln Ser Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Lys Leu Thr	
565 570 575	

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ACC AGC GGC GAT GTC AGC TGT ACT CAG ATG AAT TAC TAC TAC GGT ATG	1776
Thr Ser Gly Asp Val Ser Cys Thr Gln Met Asn Tyr Tyr Tyr Gly Met	
580 585 590	
TGT AGC AAT CCT TAT TCC GAA AAA CTG GAA TGG CAG ATG CAA AAT ATC	1824
Cys Ser Asn Pro Tyr Ser Glu Lys Leu Glu Trp Gln Met Gln Asn Ile	
595 600 605	
GAC AAG GCC AGA ATC CGC GGT ATC GAG CTG ACG GGC CGT CTG AAT GTG	1872
Asp Lys Ala Arg Ile Arg Gly Ile Glu Leu Thr Gly Arg Leu Asn Val	
610 615 620	
GAC AAA GTA GCG TCT TTT GTT CCT GAG GGC TGG AAA CTG TTC GGC TCG	1920
Asp Lys Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser	
625 630 635 640	
CTG GGT TAT GCG AAA AGC AAA CTG TCG GGC GAC AAC AGC CTG CTG TCC	1968
Leu Gly Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Ser	
645 650 655	
ACC CAG CCG TTG AAA GTG ATT GCC GGT ATC GAC TAT GAA AGT CCG AGC	2016
Thr Gln Pro Leu Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser	
660 665 670	
GAA AAA TGG GGC GTG TTC TCC CGC CTG ACC TAT CTG GGC GCG AAA AAG	2064
Glu Lys Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys	
675 680 685	
GTC AAA GAC GCG CAA TAC ACC GTT TAT GAA AAC AAG GGC TGG GGT ACG	2112
Val Lys Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Trp Gly Thr	
690 695 700	
CCT TTG CAG AAA AAG GTA AAA GAT TAC CCG TGG CTG AAC AAG TCG GCT	2160
Pro Leu Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala	
705 710 715 720	
TAT GTG TTC GAT ATG TAC GGC TTC TAC AAA CCG GTG AAA AAC CTG ACT	2208
Tyr Val Phe Asp Met Tyr Gly Phe Tyr Lys Pro Val Lys Asn Leu Thr	
725 730 735	
TTG CGT GCA GGC GTA TAT AAT GTG TTC AAC CGC AAA TAC ACC ACT TGG	2256
Leu Arg Ala Gly Val Tyr Asn Val Phe Asn Arg Lys Tyr Thr Thr Trp	
740 745 750	
GAT TCC CTG CGC GGC CTG TAT AGC TAC AGC ACC ACC AAC TCG GTC GAC	2304
Asp Ser Leu Arg Gly Leu Tyr Ser Tyr Ser Thr Thr Asn Ser Val Asp	
755 760 765	
CGC GAT GGC AAA GGC TTA GAC CGC TAC CGC GCC CCA AGC CGT AAT TAC	2352
Arg Asp Gly Lys Gly Leu Asp Arg Tyr Arg Ala Pro Ser Arg Asn Tyr	
770 775 780	
GCC GTA TCG CTG GAA TGG AAG TTT TAA	2379
Ala Val Ser Leu Glu Trp Lys Phe	
785 790	

(2) INFORMATION FOR SEQ ID NO:6:

006160" 85E5960

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 792 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Lys Pro Leu Gln Met Leu Pro Ile Ala Ala Leu Val Gly Ser Ile
1 5 10 15
Phe Gly Asn Pro Val Phe Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr
20 25 30
Pro Val Lys Ala Glu Val Lys Ala Val Arg Val Lys Gly Gln Arg Asn
35 40 45
Ala Pro Ala Ala Val Glu Arg Val Asn Leu Asn Arg Ile Lys Gln Glu
50 55 60
Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly
65 70 75 80
Leu Ser Asp Ser Gly Arg His Gln Lys Gly Phe Ala Val Arg Gly Val
85 90 95
Glu Gly Asn Arg Val Gly Val Ser Ile Asp Gly Val Asn Leu Pro Asp
100 105 110
Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser
115 120 125
Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Asp Ile Val Lys
130 135 140
Gly Ala Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly Gly Gly Val
145 150 155 160
Asn Tyr Gln Thr Leu Gln Gly Arg Asp Leu Leu Leu Pro Glu Arg Gln
165 170 175
Phe Gly Val Met Met Lys Asn Gly Tyr Ser Thr Arg Asn Arg Glu Trp
180 185 190
Thr Asn Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala
195 200 205
Leu Leu Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Lys
210 215 220
Arg Gly Tyr Pro Val Glu Gly Ala Gly Ser Gly Ala Asn Ile Arg Gly
225 230 235 240
Ser Ala Arg Gly Ile Pro Asp Pro Ser Gln His Lys Tyr His Ser Phe
245 250 255
Leu Gly Lys Ile Ala Tyr Gln Ile Asn Asp Asn His Arg Ile Gly Ala

006T60" 85259950

	260		265		270										
Ser	Leu	Asn	Gly	Gln	Gln	Gly	His	Asn	Tyr	Thr	Val	Glu	Glu	Ser	Tyr
	275						280					285			
Asn	Leu	Leu	Ala	Ser	Tyr	Trp	Arg	Glu	Ala	Asp	Asp	Val	Asn	Arg	Arg
	290					295					300				
Arg	Asn	Thr	Asn	Leu	Phe	Tyr	Glu	Trp	Thr	Pro	Glu	Ser	Asp	Arg	Leu
305					310					315					320
Ser	Met	Val	Lys	Ala	Asp	Val	Asp	Tyr	Gln	Lys	Thr	Lys	Val	Ser	Ala
				325					330					335	
Val	Asn	Tyr	Lys	Gly	Ser	Phe	Pro	Ile	Glu	Asp	Ser	Ser	Thr	Leu	Thr
			340					345					350		
Arg	Asn	Tyr	Asn	Gln	Lys	Asp	Leu	Asp	Glu	Ile	Tyr	Asn	Arg	Ser	Met
	355						360					365			
Asp	Thr	Arg	Phe	Lys	Arg	Ile	Thr	Leu	Arg	Leu	Asp	Ser	His	Pro	Leu
	370					375					380				
Gln	Leu	Gly	Gly	Gly	Arg	His	Arg	Leu	Ser	Phe	Lys	Thr	Phe	Ala	Ser
385					390					395					400
Arg	Arg	Asp	Phe	Glu	Asn	Leu	Asn	Arg	Asp	Tyr	Tyr	Tyr	Phe	Ser	Gly
				405					410					415	
Arg	Val	Val	Arg	Thr	Thr	Ser	Ser	Ile	Gln	His	Pro	Val	Lys	Thr	Thr
				420				425					430		
Asn	Tyr	Gly	Phe	Ser	Leu	Ser	Asp	Gln	Ile	Gln	Trp	Asn	Asp	Val	Phe
	435						440					445			
Ser	Ser	Arg	Ala	Gly	Ile	Arg	Tyr	Asp	His	Thr	Lys	Met	Thr	Pro	Gln
	450					455					460				
Glu	Leu	Asn	Ala	Glu	Cys	His	Ala	Cys	Asp	Lys	Thr	Pro	Pro	Ala	Ala
465					470				475						480
Asn	Thr	Tyr	Lys	Gly	Trp	Ser	Gly	Phe	Val	Gly	Leu	Ala	Ala	Gln	Leu
				485					490					495	
Asn	Gln	Ala	Trp	Arg	Val	Gly	Tyr	Asp	Ile	Thr	Ser	Gly	Tyr	Arg	Val
			500					505					510		
Pro	Asn	Ala	Ser	Glu	Val	Tyr	Phe	Thr	Tyr	Asn	His	Gly	Ser	Gly	Asn
	515						520					525			
Trp	Leu	Pro	Asn	Pro	Asn	Leu	Lys	Ala	Glu	Arg	Ser	Thr	Thr	His	Thr
	530					535					540				
Leu	Ser	Leu	Gln	Gly	Arg	Ser	Glu	Lys	Gly	Thr	Leu	Asp	Ala	Asn	Leu
545					550					555					560
Tyr	Gln	Ser	Asn	Tyr	Arg	Asn	Phe	Leu	Ser	Glu	Glu	Gln	Lys	Leu	Thr

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565	570	575
Thr Ser Gly Asp Val Ser Cys Thr Gln Met Asn Tyr Tyr Tyr Gly Met		
580	585	590
Cys Ser Asn Pro Tyr Ser Glu Lys Leu Glu Trp Gln Met Gln Asn Ile		
595	600	605
Asp Lys Ala Arg Ile Arg Gly Ile Glu Leu Thr Gly Arg Leu Asn Val		
610	615	620
Asp Lys Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser		
625	630	635
Leu Gly Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Ser		
645	650	655
Thr Gln Pro Leu Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser		
660	665	670
Glu Lys Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys		
675	680	685
Val Lys Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Trp Gly Thr		
690	695	700
Pro Leu Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala		
705	710	715
Tyr Val Phe Asp Met Tyr Gly Phe Tyr Lys Pro Val Lys Asn Leu Thr		
725	730	735
Leu Arg Ala Cly Val Tyr Asn Val Phe Asn Arg Lys Tyr Thr Thr Trp		
740	745	750
Asp Ser Leu Arg Gly Leu Tyr Ser Tyr Ser Thr Thr Asn Ser Val Asp		
755	760	765
Arg Asp Gly Lys Gly Leu Asp Arg Tyr Arg Ala Pro Ser Arg Asn Tyr		
770	775	780
Ala Val Ser Leu Glu Trp Lys Phe		
785	790	

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..2370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG AAA CCA TTA CAC ATG CTT CCT ATT GCC GCG CTG GTC GGC AGT ATT	48
Met Lys Pro Leu His Met Leu Pro Ile Ala Ala Leu Val Gly Ser Ile	
1 5 10 15	
TTC GGC AAT CCG GTC TTG GCA GCG GAT GAA GCT GCA ACC GAA ACC ACA	96
Phe Gly Asn Pro Val Leu Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr	
20 25 30	
CCC GTT AAA GCA GAG ATA AAA GAA GTG CGC GTT AAA GAC CAG CTT AAT	144
Pro Val Lys Ala Glu Ile Lys Glu Val Arg Val Lys Asp Gln Leu Asn	
35 40 45	
GCG CCT GCA ACC GTG GAA CGT GTC AAC CTC GGC CGC ATT CAA CAG GAA	192
Ala Pro Ala Thr Val Glu Arg Val Asn Leu Gly Arg Ile Gln Gln Glu	
50 55 60	
ATG ATA CGC GAC AAC AAA GAC TTG GTG CGT TAC TCC ACC GAC GTC GGC	240
Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly	
65 70 75 80	
TTG AGC GAT AGC GGC CGC CAT CAA AAA GGC TTT GCT GTG CGC GGC GTG	288
Leu Ser Asp Ser Gly Arg His Gln Lys Gly Phe Ala Val Arg Gly Val	
85 90 95	
GAA GGC AAC CGT GTC GGT GTC AGC ATT GAC GGC GTG AGC CTG CCT GAT	336
Glu Gly Asn Arg Val Gly Val Ser Ile Asp Gly Val Ser Leu Pro Asp	
100 105 110	
TCG GAA GAA AAC TCA CTG TAT GCA CGT TAT GGC AAC TTC AAC AGC TCG	384
Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser	
115 120 125	
CGC CTG TCT ATC GAC CCC GAA CTC GTG CGC AAC ATC GAA ATC GCG AAG	432
Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Glu Ile Ala Lys	
130 135 140	
GGC GCT GAC TCT TTC AAT ACC GGT AGC GGC GCA TTG GGT GGC GGC GTG	480
Gly Ala Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly Gly Gly Val	
145 150 155 160	
AAT TAC CAA ACC CTG CAA GGA CAT GAT TTG CTG TTG GAC GAC AGG CAA	528
Asn Tyr Gln Thr Leu Gln Gly His Asp Leu Leu Asp Asp Arg Gln	
165 170 175	
TTC GGC GTG ATG ATG AAA AAC GGT TAC AGC ACG CGC AAC CGC GAA TGG	576
Phe Gly Val Met Met Lys Asn Gly Tyr Ser Thr Arg Asn Arg Glu Trp	
180 185 190	
ACA AAT ACA CTC GGT TTC GGT GTG AGC AAC GAC CGC GTG GAT GCC GCT	624
Thr Asn Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala	
195 200 205	
TTG CTG TAT TCG CAA CGT CGC GGT CAT GAG ACC GAA AGC GCG GGC GAG	672
Leu Leu Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Glu	

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210	215	220	
CGT GGC TAT CCG GTA GAG GGT GCT GGC AGC GGA GCA ATT ATC CGT GGT Arg Gly Tyr Pro Val Glu Gly Ala Gly Ser Gly Ala Ile Ile Arg Gly 225 230 235 240			720
TCG TCA CGC GGT ATC CCT GAT CCG TCC AAA CAC AAA TAC CAC AAC TTC Ser Ser Arg Gly Ile Pro Asp Pro Ser Lys His Lys Tyr His Asn Phe 245 250 255			768
TTG GGT AAG ATT GCT TAT CAA ATC AAC GAC AAG CAC CGC ATC GGC CCA Leu Gly Lys Ile Ala Tyr Gln Ile Asn Asp Lys His Arg Ile Gly Pro 260 265 270			816
TCG TTT AAC GGC CAG CAG GGG CAT AAT TAC ACG ATT GAA GAG TCT TAT Ser Phe Asn Gly Gln Gln Gly His Asn Tyr Thr Ile Glu Glu Ser Tyr 275 280 285			864
AAC CTG ACC GCT TCT TCC TGG CGC GAA GCC GAT GAC GTA AAC AGA CGG Asn Leu Thr Ala Ser Ser Trp Arg Glu Ala Asp Asp Val Asn Arg Arg 290 295 300			912
CGC AAT GCC AAC CTC TTT TAC GAA TGG ACG CCT GAT TCA AAT TGG CTG Arg Asn Ala Asn Leu Phe Tyr Glu Trp Thr Pro Asp Ser Asn Trp Leu 305 310 315 320			960
TCG TCT TTG AAG GCG GAT TTC GAT TAT CAG ACA ACC AAA GTG GCG GCG Ser Ser Leu Lys Ala Asp Phe Asp Tyr Gln Thr Thr Lys Val Ala Ala 325 330 335			1008
GTT AAC AAC AAA GGC TCG TTC CCG ACG GAT TAT TCC ACC TTG ACG CGC Val Asn Asn Lys Gly Ser Phe Pro Thr Asp Tyr Ser Thr Leu Thr Arg 340 345 350			1056
AAC TAT AAT CAG AAG GAT TTG GAG AAT ATA TAC AAC CGC AGC ATG GAC Asn Tyr Asn Gln Lys Asp Leu Glu Asn Ile Tyr Asn Arg Ser Met Asp 355 360 365			1104
ACC CGA TTC AAA CGT TTT ACT TTG CGT ATG GAC AGC CAA CCG TTG CAA Thr Arg Phe Lys Arg Phe Thr Leu Arg Met Asp Ser Gln Pro Leu Gln 370 375 380			1152
CTG GGC GGC CAA CAT CGC TTG TCG CTT AAA ACT TTC GCC AGT CGG CGT Leu Gly Gly Gln His Arg Leu Ser Leu Lys Thr Phe Ala Ser Arg Arg 385 390 395 400			1200
GAG TTT GAA AAC TTA AAC CGC GAC GAT TAT TAC TTC AGC GAA AGA GTA Glu Phe Glu Asn Leu Asn Arg Asp Asp Tyr Tyr Phe Ser Glu Arg Val 405 410 415			1248
TCC CGT ACT ACC AGC TCG ATT CAA CAC CCC GTG AAA ACC ACT AAT TAT Ser Arg Thr Thr Ser Ser Ile Gln His Pro Val Lys Thr Thr Asn Tyr 420 425 430			1296
GGT TTC TCA CTG TCT GAT CAA ATC CAA TGG AAC GAC GTG TTC AGC AGC Gly Phe Ser Leu Ser Asp Gln Ile Gln Trp Asn Asp Val Phe Ser Ser 435 440 445			1344
CGT GCA GAT ATC CGT TAC GAT CAT ACC AAA ATG ACG CCT CAG GAA TTG			1392

006760" 85259960

Arg	Ala	Asp	Ile	Arg	Tyr	Asp	His	Thr	Lys	Met	Thr	Pro	Gln	Glu	Leu	
450						455					460					
AAT	GCC	GAG	TGT	CAT	GCT	TGT	GAC	AAA	ACA	CCG	CCT	GCA	GCC	AAT	ACT	1440
Asn	Ala	Glu	Cys	His	Ala	Cys	Asp	Lys	Thr	Pro	Pro	Ala	Ala	Asn	Thr	
465					470					475					480	
TAT	AAA	GGC	TGG	AGC	GGA	TTT	GTC	GGT	TTG	GCG	GCG	CAA	CTG	AAT	CAG	1488
Tyr	Lys	Gly	Trp	Ser	Gly	Phe	Val	Gly	Leu	Ala	Ala	Gln	Leu	Asn	Gln	
				485					490						495	
GCT	TGG	CAT	GTC	GGT	TAC	GAC	ATT	ACT	TCC	GGC	TAC	CGT	GTC	CCC	AAT	1536
Ala	Trp	His	Val	Gly	Tyr	Asp	Ile	Thr	Ser	Gly	Tyr	Arg	Val	Pro	Asn	
			500					505					510			
GCG	TCC	GAA	GTG	TAT	TTC	ACT	TAC	AAC	CAC	GGT	TCG	GGT	AAT	TGG	CTG	1584
Ala	Ser	Glu	Val	Tyr	Phe	Thr	Tyr	Asn	His	Gly	Ser	Gly	Asn	Trp	Leu	
		515					520					525				
CCC	AAT	CCC	AAC	CTG	AAA	GCC	GAG	CGC	AGC	ACC	ACC	CAC	ACC	CTG	TCT	1632
Pro	Asn	Pro	Asn	Leu	Lys	Ala	Glu	Arg	Ser	Thr	Thr	His	Thr	Leu	Ser	
	530					535					540					
CTG	CAA	GGC	CGC	AGC	GAA	AAA	GGT	ACT	TTG	GAT	GCC	AAC	CTG	TAT	CAA	1680
Leu	Gln	Gly	Arg	Ser	Glu	Lys	Gly	Thr	Leu	Asp	Ala	Asn	Leu	Tyr	Gln	
545					550					555					560	
AGC	AAT	TAC	CGA	AAC	TTC	TTG	TCT	GAA	GAG	CAG	AAG	CTG	ACC	ACC	AGC	1728
Ser	Asn	Tyr	Arg	Asn	Phe	Leu	Ser	Glu	Gln	Lys	Leu	Thr	Thr	Thr	Ser	
				565					570						575	
GGC	GAT	GTC	GGC	TGT	ACT	CAG	ATG	AAT	TAC	TAC	TAC	GGT	ATG	TGT	AGC	1776
Gly	Asp	Val	Gly	Cys	Thr	Gln	Met	Asn	Tyr	Tyr	Tyr	Gly	Met	Cys	Ser	
			580					585					590			
AAT	CCT	TAT	TCC	GAA	AAA	CCG	GAA	TGG	CAG	ATG	CAA	AAT	ATC	GAT	AAG	1824
Asn	Pro	Tyr	Ser	Glu	Lys	Pro	Glu	Trp	Gln	Met	Gln	Asn	Ile	Asp	Lys	
		595					600					605				
GCC	CGA	ATC	CGT	GGT	CTT	GAG	CTG	ACG	GGC	CGT	CTG	AAT	GTG	ACA	AAA	1872
Ala	Arg	Ile	Arg	Gly	Leu	Glu	Leu	Thr	Gly	Arg	Leu	Asn	Val	Thr	Lys	
	610					615					620					
GTA	GCG	TCT	TTT	GTT	CCT	GAG	GGC	TGG	AAA	TTG	TTC	GGC	TCG	CTG	GGT	1920
Val	Ala	Ser	Phe	Val	Pro	Glu	Gly	Trp	Lys	Leu	Phe	Gly	Ser	Leu	Gly	
625					630					635					640	
TAT	GCG	AAA	AGC	AAA	CTG	TCG	GGC	GAC	AAC	AGC	CTG	CTG	TCC	ACA	CAG	1968
Tyr	Ala	Lys	Ser	Lys	Leu	Ser	Gly	Asp	Asn	Ser	Leu	Leu	Ser	Thr	Gln	
				645					650						655	
CCG	CCG	AAA	GTG	ATT	GCC	GGT	ATC	GAC	TAT	GAA	AGT	CCG	AGC	GAA	AAA	2016
Pro	Pro	Lys	Val	Ile	Ala	Gly	Ile	Asp	Tyr	Glu	Ser	Pro	Ser	Glu	Lys	
			660					665					670			
TGG	GGT	GTG	TTC	TCC	CGC	CTG	ACT	TAT	CTG	GGT	GCG	AAA	AAG	GTC	AAA	2064
Trp	Gly	Val	Phe	Ser	Arg	Leu	Thr	Tyr	Leu	Gly	Ala	Lys	Lys	Val	Lys	
		675					680					685				

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GAC GCG CAA TAC ACC GTT TAT GAA AAC AAG GGC CGG GGT ACG CCT TTG	2112
Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Arg Gly Thr Pro Leu	
690 695 700	
CAG AAA AAG GTA AAA GAT TAC CCG TGG CTG AAC AAG TCG GCT TAT GTG	2160
Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala Tyr Val	
705 710 715 720	
TTT GAT ATG TAC GGC TTC TAC AAA CTG GCT AAA AAC CTG ACT TTG CGT	2208
Phe Asp Met Tyr Gly Phe Tyr Lys Leu Ala Lys Asn Leu Thr Leu Arg	
725 730 735	
GCA GGC GTA TAT AAT GTG TTC AAC CGC AAA TAC ACC ACT TGG GAT TCC	2256
Ala Gly Val Tyr Asn Val Phe Asn Arg Lys Tyr Thr Thr Trp Asp Ser	
740 745 750	
CTG CGC GGT TTG TAT AGC TAC ACC ACC ACC AAC GCG GTC GAC CGA GAT	2304
Leu Arg Gly Leu Tyr Ser Tyr Thr Thr Thr Asn Ala Val Asp Arg Asp	
755 760 765	
GGC AAA GGC TTA GAC CGC TAC CGC GCC TCA GGC CGT AAT TAC GCC GTA	2352
Gly Lys Gly Leu Asp Arg Tyr Arg Ala Ser Gly Arg Asn Tyr Ala Val	
770 775 780	
TCG CTG GAT TGG AAG TTT TGAATTCC	2378
Ser Leu Asp Trp Lys Phe	
885 790	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Lys Pro Leu His Met Leu Pro Ile Ala Ala Leu Val Gly Ser Ile	
1 5 10 15	
Phe Gly Asn Pro Val Leu Ala Ala Asp Glu Ala Ala Thr Glu Thr Thr	
20 25 30	
Pro Val Lys Ala Glu Ile Lys Glu Val Arg Val Lys Asp Gln Leu Asn	
35 40 45	
Ala Pro Ala Thr Val Glu Arg Val Asn Leu Gly Arg Ile Gln Gln Glu	
50 55 60	
Met Ile Arg Asp Asn Lys Asp Leu Val Arg Tyr Ser Thr Asp Val Gly	
65 70 75 80	
Leu Ser Asp Ser Gly Arg His Gln Lys Gly Phe Ala Val Arg Gly Val	
85 90 95	
Glu Gly Asn Arg Val Gly Val Ser Ile Asp Gly Val Ser Leu Pro Asp	

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100	105	110
Ser Glu Glu Asn Ser Leu Tyr Ala Arg Tyr Gly Asn Phe Asn Ser Ser	115	120
Arg Leu Ser Ile Asp Pro Glu Leu Val Arg Asn Ile Glu Ile Ala Lys	130	135
Gly Ala Asp Ser Phe Asn Thr Gly Ser Gly Ala Leu Gly Gly Gly Val	145	150
Asn Tyr Gln Thr Leu Gln Gly His Asp Leu Leu Leu Asp Asp Arg Gln	165	170
Phe Gly Val Met Met Lys Asn Gly Tyr Ser Thr Arg Asn Arg Glu Trp	180	185
Thr Asn Thr Leu Gly Phe Gly Val Ser Asn Asp Arg Val Asp Ala Ala	195	200
Leu Leu Tyr Ser Gln Arg Arg Gly His Glu Thr Glu Ser Ala Gly Glu	210	215
Arg Gly Tyr Pro Val Glu Gly Ala Gly Ser Gly Ala Ile Ile Arg Gly	225	230
Ser Ser Arg Gly Ile Pro Asp Pro Ser Lys His Lys Tyr His Asn Phe	245	250
Leu Gly Lys Ile Ala Tyr Gln Ile Asn Asp Lys His Arg Ile Gly Pro	260	265
Ser Phe Asn Gly Gln Gln Gly His Asn Tyr Thr Ile Glu Glu Ser Tyr	275	280
Asn Leu Thr Ala Ser Ser Trp Arg Glu Ala Asp Asp Val Asn Arg Arg	290	295
Arg Asn Ala Asn Leu Phe Tyr Glu Trp Thr Pro Asp Ser Asn Trp Leu	305	310
Ser Ser Leu Lys Ala Asp Phe Asp Tyr Gln Thr Thr Lys Val Ala Ala	325	330
Val Asn Asn Lys Gly Ser Phe Pro Thr Asp Tyr Ser Thr Leu Thr Arg	340	345
Asn Tyr Asn Gln Lys Asp Leu Glu Asn Ile Tyr Asn Arg Ser Met Asp	355	360
Thr Arg Phe Lys Arg Phe Thr Leu Arg Met Asp Ser Gln Pro Leu Gln	370	375
Leu Gly Gly Gln His Arg Leu Ser Leu Lys Thr Phe Ala Ser Arg Arg	385	390
Glu Phe Glu Asn Leu Asn Arg Asp Asp Tyr Tyr Phe Ser Glu Arg Val	405	410

005760" B5E5960

Ser Arg Thr Thr Ser Ser Ile Gln His Pro Val Lys Thr Thr Asn Tyr
420 425 430

Gly Phe Ser Leu Ser Asp Gln Ile Gln Trp Asn Asp Val Phe Ser Ser
435 440 445

Arg Ala Asp Ile Arg Tyr Asp His Thr Lys Met Thr Pro Gln Glu Leu
450 455 460

Asn Ala Glu Cys His Ala Cys Asp Lys Thr Pro Pro Ala Ala Asn Thr
465 470 475 480

Tyr Lys Gly Trp Ser Gly Phe Val Gly Leu Ala Ala Gln Leu Asn Gln
485 490 495

Ala Trp His Val Gly Tyr Asp Ile Thr Ser Gly Tyr Arg Val Pro Asn
500 505 510

Ala Ser Glu Val Tyr Phe Thr Tyr Asn His Gly Ser Gly Asn Trp Leu
515 520 525

Pro Asn Pro Asn Leu Lys Ala Glu Arg Ser Thr Thr His Thr Leu Ser
530 535 540

Leu Gln Gly Arg Ser Glu Lys Gly Thr Leu Asp Ala Asn Leu Tyr Gln
545 550 555 560

Ser Asn Tyr Arg Asn Phe Leu Ser Glu Glu Gln Lys Leu Thr Thr Ser
565 570 575

Gly Asp Val Gly Cys Thr Gln Met Asn Tyr Tyr Tyr Gly Met Cys Ser
580 585 590

Asn Pro Tyr Ser Glu Lys Pro Glu Trp Gln Met Gln Asn Ile Asp Lys
595 600 605

Ala Arg Ile Arg Gly Leu Glu Leu Thr Gly Arg Leu Asn Val Thr Lys
610 615 620

Val Ala Ser Phe Val Pro Glu Gly Trp Lys Leu Phe Gly Ser Leu Gly
625 630 635 640

Tyr Ala Lys Ser Lys Leu Ser Gly Asp Asn Ser Leu Leu Ser Thr Gln
645 650 655

Pro Pro Lys Val Ile Ala Gly Ile Asp Tyr Glu Ser Pro Ser Glu Lys
660 665 670

Trp Gly Val Phe Ser Arg Leu Thr Tyr Leu Gly Ala Lys Lys Val Lys
675 680 685

Asp Ala Gln Tyr Thr Val Tyr Glu Asn Lys Gly Arg Gly Thr Pro Leu
690 695 700

Gln Lys Lys Val Lys Asp Tyr Pro Trp Leu Asn Lys Ser Ala Tyr Val
705 710 715 720

Phe Asp Met Tyr Gly Phe Tyr Lys Leu Ala Lys Asn Leu Thr Leu Arg

005T60" 35E59960

(2) INFORMATION FOR SEQ ID NO:9:

(A) LENGTH: 600 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

Met	Gln	Gln	Gln	His	Leu	Phe	Arg	Leu	Asn	Ile	Leu	Cys	Leu	Ser	Leu
1				5					10						15
Met	Thr	Ala	Leu	Pro	Val	Tyr	Ala	Glu	Asn	Val	Gln	Ala	Glu	Gln	Ala
			20					25					30		
Gln	Glu	Lys	Gln	Leu	Asp	Thr	Ile	Val	Lys	Ala	Lys	Lys	Gln	Lys	Thr
		35					40					45			
Arg	Arg	Asp	Asn	Glu	Val	Thr	Gly	Leu	Gly	Lys	Leu	Val	Lys	Ser	Ser
	50					55					60				
Asp	Thr	Leu	Ser	Lys	Glu	Gln	Val	Leu	Asn	Ile	Arg	Asp	Leu	Thr	Arg
65					70				75						80
Tyr	Asp	Pro	Gly	Ile	Ala	Val	Val	Glu	Gln	Gly	Arg	Gly	Ala	Ser	Ser
				85					90					95	
Gly	Tyr	Ser	Ile	Arg	Gly	Met	Asp	Lys	Asn	Arg	Val	Ser	Leu	Thr	Val
			100					105					110		
Asp	Gly	Val	Ser	Gln	Ile	Gln	Ser	Tyr	Thr	Ala	Gln	Ala	Ala	Leu	Gly
	115						120					125			
Gly	Thr	Arg	Thr	Ala	Gly	Ser	Ser	Gly	Ala	Ile	Asn	Glu	Ile	Glu	Tyr
	130					135					140				
Glu	Asn	Val	Lys	Ala	Val	Glu	Ile	Ser	Lys	Gly	Ser	Asn	Ser	Ser	Glu
145					150					155					160
Tyr	Gly	Asn	Gly	Ala	Leu	Ala	Gly	Ser	Val	Ala	Phe	Gln	Thr	Lys	Thr
				165					170					175	

Ala Ala Asp Ile Ile Gly Glu Gly Lys Gln Trp Gly Ile Gln Ser Lys
180 185 190

Thr Ala Tyr Ser Gly Lys Asp His Ala Leu Thr Gln Ser Leu Ala Leu
195 200 205

Ala Gly Arg Ser Gly Gly Ala Glu Ala Leu Leu Ile Tyr Thr Lys Arg
210 215 220

Arg Gly Arg Glu Ile His Ala His Lys Asp Ala Gly Lys Gly Val Gln
225 230 235 240

Ser Phe Asn Arg Leu Pro Ile Cys Arg Phe Gly Asn Asn Thr Tyr Thr
245 250 255

Asp Cys Thr Pro Arg Asn Ile Gly Gly Asn Gly Tyr Tyr Ala Ala Val
260 265 270

Gln Asp Asn Val Arg Leu Gly Arg Trp Ala Asp Val Gly Ala Gly Ile
275 280 285

Arg Tyr Asp Tyr Arg Ser Thr His Ser Glu Asp Lys Ser Val Ser Thr
290 295 300

Gly Thr His Arg Asn Leu Ser Trp Asn Ala Gly Val Val Leu Lys Pro
305 310 315 320

Phe Thr Trp Met Asp Leu Thr Tyr Arg Ala Ser Thr Gly Phe Arg Leu
325 330 335

Pro Ser Phe Ala Glu Met Tyr Gly Trp Arg Ala Gly Glu Ser Leu Lys
340 345 350

Thr Leu Asp Leu Lys Pro Glu Lys Ser Phe Asn Arg Glu Ala Gly Ile
355 360 365

Val Phe Lys Gly Asp Phe Gly Asn Leu Glu Ala Ser Tyr Phe Asn Asn
370 375 380

Ala Tyr Arg Asp Leu Ile Ala Phe Gly Tyr Glu Thr Arg Thr Gln Asn
385 390 395 400

Gly Gln Thr Ser Ala Ser Gly Asp Pro Gly Tyr Arg Asn Ala Gln Asn
405 410 415

Ala Arg Ile Ala Gly Ile Asn Ile Leu Gly Lys Ile Asp Trp His Gly
420 425 430

Val Trp Gly Gly Leu Pro Asp Gly Leu Tyr Ser Thr Leu Ala Tyr Asn
435 440 445

Arg Ile Lys Val Lys Asp Ala Asp Arg Ala Asp Arg Thr Phe Val Thr
450 455 460

Ser Tyr Leu Phe Asp Ala Val Gln Pro Ser Arg Tyr Val Leu Gly Leu
465 470 475 480

Gly Tyr Asp His Pro Asp Gly Ile Trp Gly Ile Asn Thr Met Phe Thr
485 490 495

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See
BI
cont

Tyr Ser Lys Ala Lys Ser Val Asp Glu Leu Leu Gly Ser Gln Ala Leu
500 505 510

Leu Asn Gly Asn Ala Asn Ala Lys Lys Ala Ala Ser Arg Arg Thr Arg
515 520 525

Pro Trp Tyr Val Thr Asp Val Ser Gly Tyr Tyr Asn Ile Lys Lys His
530 535 540

Leu Thr Leu Arg Ala Gly Val Tyr Asn Leu Leu Asn Tyr Arg Tyr Val
545 550 555 560

Thr Trp Glu Asn Val Arg Gln Thr Ala Gly Gly Ala Val Asn Gln His
565 570 575

Lys Asn Val Gly Val Tyr Asn Arg Tyr Ala Ala Pro Gly Arg Asn Tyr
580 585 590

Thr Phe Ser Leu Glu Met Lys Phe
595 600

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 607 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Asn Lys Lys His Gly Phe Gln Leu Thr Leu Thr Ala Leu Ala Val
1 5 10 15

Ala Ala Ala Phe Pro Ser Tyr Ala Ala Asn Pro Glu Thr Ala Ala Pro
20 25 30

Asp Ala Ala Gln Thr Gln Ser Leu Lys Glu Val Thr Val Arg Ala Ala
35 40 45

Lys Val Gly Arg Arg Ser Lys Glu Ala Thr Gly Leu Gly Lys Ile Ala
50 55 60

Lys Thr Ser Glu Thr Leu Asn Lys Glu Gln Val Leu Gly Ile Arg Asp
65 70 75 80

Leu Thr Arg Tyr Asp Pro Gly Val Ala Val Val Glu Gln Gly Asn Gly
85 90 95

Ala Ser Gly Glu Tyr Ser Ile Arg Gly Val Asp Lys Asn Arg Val Ala
100 105 110

Val Ser Val Asp Gly Val Ala Gln Ile Gln Ala Phe Thr Val Gln Gly
115 120 125

Ser Leu Ser Gly Tyr Gly Gly Arg Gly Gly Ser Gly Ala Ile Asn Glu

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Sub
BI
cont

130		135		140
Ile Glu Tyr	Glu Asn Ile Ser Thr Val Glu Ile Asp Lys Gly Ala Gly			
145		150		155 160
Ser Ser Asp His Gly Ser Gly Ala Leu Gly Gly Ala Val Ala Phe Arg				
	165		170	175
Thr Lys Glu Ala Ala Asp Leu Ile Ser Asp Gly Lys Ser Trp Gly Ile				
	180		185	190
Gln Ala Lys Thr Ala Tyr Gly Ser Lys Asn Arg Gln Phe Met Lys Ser				
	195		200	205
Leu Gly Ala Gly Phe Ser Lys Asp Gly Trp Glu Gly Leu Leu Ile Arg				
	210		215	220
Thr Glu Arg Gln Gly Arg Glu Thr His Pro His Gly Asp Ile Ala Asp				
	225		230	235 240
Gly Val Ala Tyr Gly Ile Asn Arg Leu Ser Val Cys Gly Tyr Ile Glu				
	245		250	255
Thr Leu Arg Ser Arg Lys Cys Val Pro Arg Lys Ile Asn Gly Ser Asn				
	260		265	270
Ile His Ile Ser Leu Asn Asp Arg Phe Ser Ile Gly Lys Tyr Phe Asp				
	275		280	285
Phe Ser Leu Gly Gly Arg Tyr Asp Arg Lys Asn Phe Thr Thr Ser Glu				
	290		295	300
Glu Leu Val Arg Ser Gly Arg Tyr Val Asp Arg Ser Trp Asn Ser Gly				
	305		310	315 320
Ile Val Phe Lys Pro Asn Arg His Phe Ser Leu Ser Tyr Arg Ala Ser				
	325		330	335
Ser Gly Phe Arg Thr Pro Ser Phe Gln Glu Leu Phe Gly Ile Asp Ile				
	340		345	350
Tyr His Asp Tyr Pro Lys Gly Trp Gln Arg Pro Ala Leu Lys Ser Glu				
	355		360	365
Lys Ala Ala Asn Arg Glu Ile Gly Leu Gln Trp Lys Gly Asp Phe Gly				
	370		375	380
Phe Leu Glu Ile Ser Ser Phe Arg Asn Arg Tyr Thr Asp Met Ile Ala				
	385		390	395 400
Val Ala Asp His Lys Thr Lys Leu Pro Asn Gln Ala Gly Gln Leu Thr				
	405		410	415
Glu Ile Asp Ile Arg Asp Tyr Tyr Asn Ala Gln Asn Met Ser Leu Gln				
	420		425	430
Gly Val Asn Ile Leu Gly Lys Ile Asp Trp Asn Gly Val tyr Gly Lys				
	435		440	445

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*Sub
B1
cont*

Leu Pro Glu Gly Leu Tyr Thr Thr Leu Ala Tyr Asn Arg Ile Lys Pro
450 455 460

Lys Ser Val Ser Asn Arg Pro Gly Leu Ser Leu Arg Ser Tyr Ala Leu
465 470 475 480

Asp Ala Val Gln Pro Ser Arg Tyr Val Leu Gly Phe Gly Tyr Asp Gln
485 490 495

Pro Glu Gly Lys Trp Gly Ala Asn Ile Met Leu Thr Tyr Ser Lys Gly
500 505 510

Lys Asn Pro Asp Glu Leu Ala Tyr Leu Ala Gly Asp Gln Lys Arg Tyr
515 520 525

Ser Thr Lys Arg Ala Ser Ser Ser Trp Ser Thr Ala Asp Val Ser Ala
530 535 540

Tyr Leu Asn Leu Lys Lys Arg Leu Thr Leu Arg Ala Ala Ile Tyr Asn
545 550 555 560

Ile Gly Asn Tyr Arg Tyr Val Thr Trp Glu Ser Leu Arg Gln Thr Ala
565 570 575

Glu Ser Thr Ala Asn Arg His Gly Gly Asp Ser Asn Tyr Gly Arg Tyr
580 585 590

Ala Ala Pro Gly Arg Asn Phe Ser Leu Ala Leu Gly Met Lys Phe
595 600 605

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAACAGGTCT CGGCATAG

18

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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See B1 cont

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGCGAATTCA AACAGGTCTC GGCATAG

27

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGCGAATTCA AAAACTTCCA TTCCAGCGAT ACG

33

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TAAAACTTCC ATTCCAGCGA TACG

24

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B1